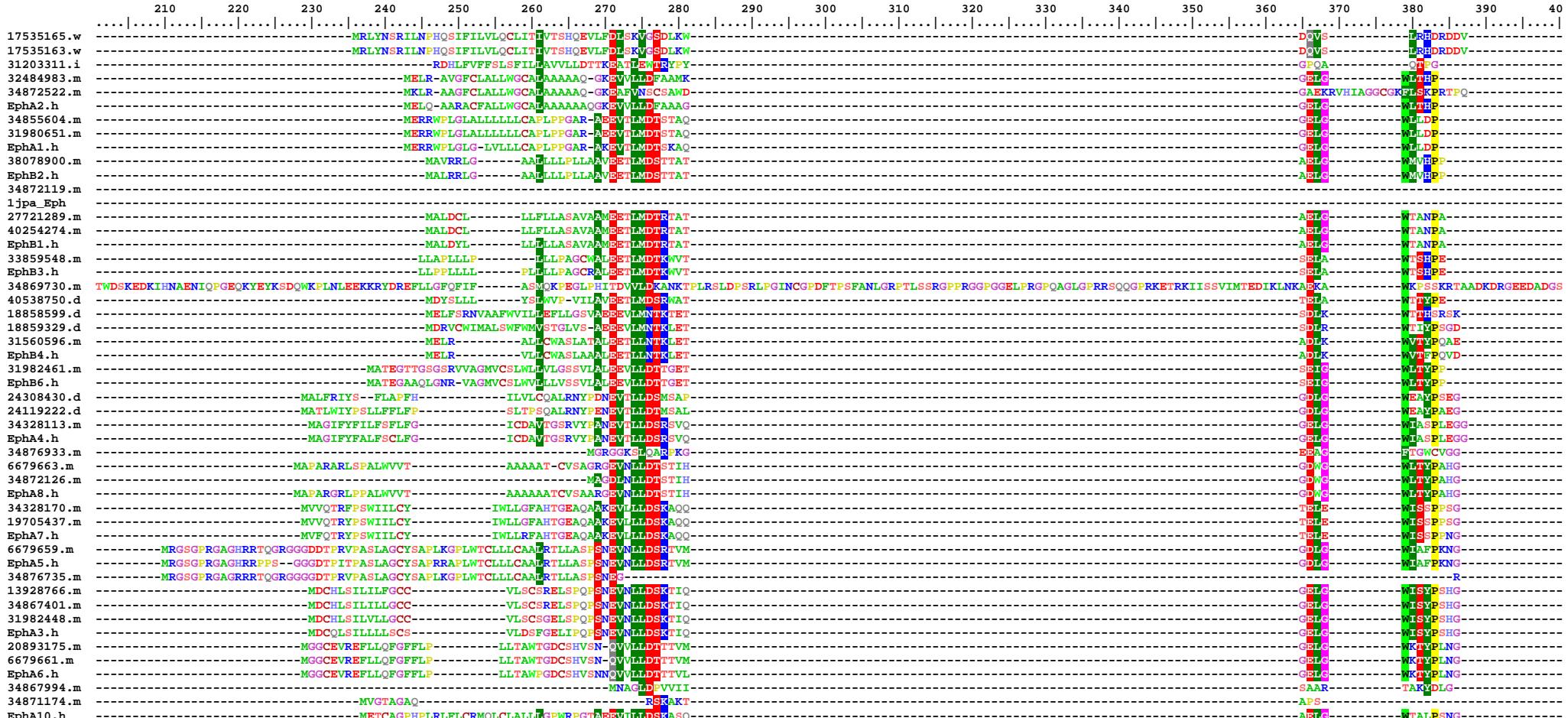
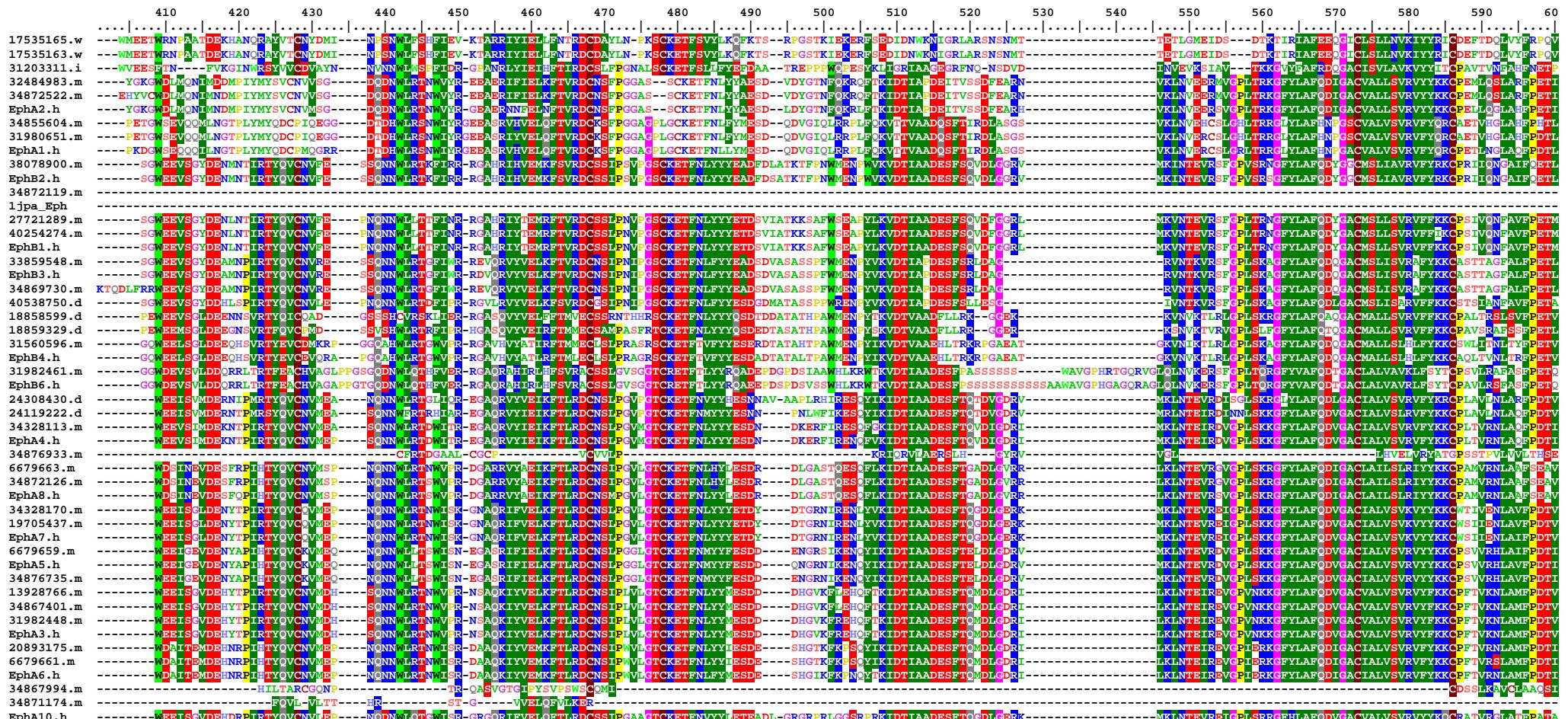


Eph A and B family kinases

|← . . . Jun-like transcription factor (E=.38) →|



|← Ephrin receptor ligand binding domain . . .



. . Ephrin ligand binding domain



17535165.w TG-PKEPD**MVRMNGSCLPNAK**KIPGVD-LIGLCMS**TSGH-KTS**ECV**CDS**TS**IADSN**GARCESCPNTYKPKQSLCKSCPSNS**ISSEAA**S-SRC**LN**TYFRAED**E**LISMPCTO-PPSRPIKLVANAITA-TSTRLSNEPS-SLGGCPEIINMEVKGSRG-EGCTVV
 17535163.w TG-PKEPD**MVRMNGSCLPNAK**KIPGVD-LIGLCMS**TSGH-KTS**ECV**CDS**TS**IADSN**GARCESCPNTYKPKQSLCKSCPSNS**ISSEAA**S-SRC**LN**TYFRAED**E**LISMPCTO-PPSRPIKLVANAITA-TSTRLSNEPS-SLGGCPEIINMEVKGSRG-EGCTVV
 31203311.i TG-RE**T**IE**E**Q**O**MGCV**V**ENAP**E**YER-PTYLCK**D**KW**I**-IL**G**GR**R**K**V****E**PDAE**K**-QTC**N**VC**V****E**R**S**A**R**T**C**I**P**L**N**K**T**N**V****S**P**C**P**L**S**H**R**F**R**O**K**M**P**C**K**M**PP**G**P**H****I**N**T**L**F**D**Q**-TS**A**IL**E**W**N**A**Q**R**A**D**E**Q**L**D**S**K**R****S**P**I**V**R****V****R****C**A**T**-SN-VVF
 32484983. AVAVSD**I**Q**P**LA**T**VA**G**T**C**V**D**IA**V**V**P**Y**G**GE**G**-P**I**M**H**C**V****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-V**E****D****A****C****R****A****S****P****I****E****F****F****E****A****S**-E**S****P****C****L****O****C****E****H****I****L****P****S****T****E****C****A****T****S****C****Q****C****E****T****V****F****R****A****P****E****D****L****S****M****S****C****T****R****P****P****S****A****P****H****Y****L****T****A****I****G****M****G**-AK**V****E****L****R****T****A****P****Q**-DT**G****G****R****K****D****I****V****S****V****I****C****E****O****W**-P**E****S****G****E****C****G****I****C****E****A****S****V****Y**
 34872522.m AVAVSD**I**Q**P**LA**T**VA**G**T**C**V**D**IA**V**V**P**Y**G**GE**G**-P**I**M**H**C**V****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-V**E****D****A****C****R****A****S****P****I****E****F****F****E****A****S**-E**S****P****C****L****O****C****E****H****I****L****P****S****T****E****C****A****T****S****C****Q****C****E****T****V****F****R****A****P****E****D****L****S****M****S****C****T****R****P****P****S****A****P****H****Y****L****T****A****I****G****M****G**-AK**V****E****L****R****T****A****P****Q**-DT**G****G****R****K****D****I****V****S****V****I****C****E****O****W**-P**E****S****G****E****C****G****I****C****E****A****S****V****Y**
 EphA2.h AG-S**D****A****S****I****A****T****V****A****G**T**C**V**D**IA**V**V**P**Y**G**GE**G**-PR**M****H**C**F****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-V**E****D****A****C****R****A****S****P****I****E****F****F****E****A****S**-E**S****P****C****L****O****C****E****H****I****L****P****S****T****E****C****A****T****S****C****Q****C****E****T****V****F****R****A****P****E****D****L****S****M****S****C****T****R****P****P****S****A****P****H****Y****L****T****A****I****G****M****G**-AK**V****E****L****R****T****A****P****Q**-D**S****G****E****D****I****V****N****I****C****K****S****G****S**-P**E****S****G****E****C****G****I****C****E****A****S****V****Y**
 34855604.m PG-**F**G**L****V****E****V****A****G**T**C**L**S****H****A****Q****I****S****G****S****G**-PR**M****H**C**F****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-OD**G****G****C****Q****E****C****G****K****V****F**
 31980651.m PG-**F**G**L****V****E****V****A****G**T**C**L**S****H****A****Q****I****S****G****S****G**-PR**M****H**C**F****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-OD**G****G****C****Q****E****C****G****K****V****F**
 EphA1.h PG-**F**G**L****V****E****V****A****G**T**C**L**S****H****A****Q****I****S****G****S****G**-PR**M****H**C**F****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-OD**G****G****C****Q****E****C****G****K****V****F**
 38078900.m SG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****D****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DS**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-R**G****A****C****T****R****G****D****N****V****Y**
 EphB2.h SG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****D****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DS**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-R**G****A****C****T****R****G****D****N****V****Y**
 34872119.m 1jpa_Eph
 2771289. TG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****D****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-RR**S****C****F****R****D****N****V****Y**
 40254274.m TG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****D****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-RR**S****C****F****R****D****N****V****Y**
 EphB1.h TG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****D****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****R****Y****V****E****C****L****O****R****G****I****A**-RR**S****C****F****R****D****N****V****Y**
 33859548.m TG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****S****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****L****Y****V****N****I****C****K****G****R****S****G****S****G****G****A****D****-****R****R****S****C****F****R****D****N****V****Y**
 EphB3.h TG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****S****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****L****Y****V****N****I****C****K****G****R****S****G****S****G****G****A****D****-****R****R****S****C****F****R****D****N****V****Y**
 34869730.m TG-AE**T**SL**V****A****R****G****S****C****I****N****A****E****V****S****V**-PI**K****L****C****N****G****D****E****M****I**-V**I**G**O**C**L****O**E**E****Y****E****K**-C**P****Y****E****E****S****G****S****V****G****C****T****A****C****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****L****Y****V****N****I****C****K****G****R****S****G****S****G****G****A****D****-****R****R****S****C****F****R****D****N****V****Y**
 40538750.d TG-AD**S****A****L****E****V****R****G****C****N****V****N****S****V****D**-V**D****G****C****O****R****S****E****A****S****P****T****E****F****Y****R****D****M****N**-T**I****L****H****C****K****Q****H****S****V****A****E****S****T****I****C****T****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****L****Y****V****N****I****C****K****G****R****S****G****S****G****G****A****D****-****R****R****S****C****F****R****D****N****V****Y**
 18855859.m PG-**F****I****S****L****V****E****G****C****N****V****N****S****V****D**-R**P****K****M****F****C****D****G****M****D**-T**R****C****A****G****L****D****P****T****C****I****T****P****R****S****I****I****Q****N****D**-T**W****V****L****E****S****P****L****E****P****R****D****I****L****T****V****N****I****C****E****N****G****Y****H****R****A****C****P****C****V****A****C****T****R****P****P****S****A****N****O****L****S****I****S****A****S**-T**Q****E****S****L****R****E****P****R**-DT**G****G****R****D****I****L****Y****V****N****I****C**<b

. . fn 3 domain .→|

| ← fn 3 domain . . .

1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 12

 17535165.w DNPETVYQFRVRIRDRLRWSQ--PISYQLGRGLMSPPSSNE--VEESQFLNQTGSALLIHALILILIVIAVLCMIVVQK--NSKNRKOMSDDLVLDYKQDSMTPDYHTTSRHRRHQQNLPATLHEQLRSTTKLNAPLIPSGS--PISQPPYYGGVHFN--
 17535163.w DNPETVYQFRVRIRDRLRWSQ--PISYQLGRGLMSPPSSNE--VEESQFLNQTGSALLIHALILILIVIAVLCMIVVQK--NSKNRKOMSDDLVLDYKQDSMTPDYHTTSRHRRHQQNLPATLHEQLRSTTKLNAPLIPSGS--PISQPPYYGGVHFN--
 31203311.i VWDKPINSDPIEYEVWRWP--KSEVDAMNSSVLSIKEEK--VHIGDLLENT-EYGFQVRCCKTENGWGTFSNIVYACT--HQSVSPVYDDSFQHIVAGTTVTVFILVLVIVITVVFLRSKNHDEIDKKTNHPLPMYDASNEVHAMDTTIVVKTMKSNVITPLF
 32484983.m LDDIAPDPITYLWVVOAQTQEG--QAGSKVIEFOILSSTEKS--ANMAVIGGVAVGVVLLVLILAG--VGLIIRRRLNLRARQSED--VRFSKSEQ--L
 34872522.m LDDIAPDPITYLWVVOAQTQEG--QAGSKVIEFOILSSTEKS--ATMAVIGGVAVGVVLLVLILAG--ICFFIIRRRLNLRARQSED--VRFSKSEQ--L
 EphA2.h LDDIAPDPITYLWVVOAQTQEG--QAGSKVIEFOILSSTEKS--GNLAVIGGVAVGVVLLVLILAG--VGFIIIRRRLNLRARQSED--VRFSKSEQ--L
 34855604.m LTKLQDPDTIYIVRVRTLTPEPG--PQPFSPDIEFRSP--VSRSLTGEVVAIFCLLIGIALLIGIIVVFRSRRGQ--ROROROR--ERTINVDRGEPGPYPSRALIVPLHWLS--SLVLPPLPEDK
 31980651.m LTKLQDPDTIYIVRVRTLTPEPG--PQPFSPDIEFRSP--VSRSLTGEVVAIFCLLIGIALLIGIIVVFRSRRGQ--ROROROR--ERTINVDRGEPGPYPSRALIVPLHWLS--EDK
 EphA1.h LTBLOPPDTIYIVRVRTLTPEPG--PQPFSPDIEFRSP--VSRSLTGEVVAIFCLLIGIALLIGIIVVFRSRRAQ--RORQRHVTAPPWIEPTSCAEA--LCGT
 38078900.m VQGLKAGAIKVFOVRAARTVAG--YRYSKMFMOTIMEAEY--QT-SIKEKEELIVGSSAAALVSLIIVVVIAIVCNR--RGERADSEYDQYDQYTS--GHMT
 EphB2.h VQGLKAGAIKVFOVRAARTVAG--YRYSKMFMOTIMEAEY--QT-SIKEKEELIVGSSAAALVSLIIVVVIAIVCNR--RGERADSEYDQYDQYTS--GHMT
 34872119.m
 1jpa_Eph
 27721289.n IDGHRPGMVVYVQVRAARTVAG--YCFSKMFCOTLDDY--KS-ELREQDELIAGSAAAIVVWVLLVILISIVCSR--RGRASKEAVYSDKCGPYST--GHMT
 40254274.m IDGHRPGMVVYVQVRAARTVAG--YCFSKMFCOTLDDY--KS-ELREQDELIAGSAAAIVVWVLLVILISIVCSR--RGRASKEAVYSDKCGPYST--GRGS
 EphB1.h IDGHRPGMVVYVQVRAARTVAG--YCFSKMFCOTLDDY--KS-ELREQDELIAGSAAAIVVWVLLVILISIVCSR--RGRASKEAVYSDKCGPYST--GRGS
 33859548.m IDGLOPDARZVWVQVRAARTVAG--YCOYSRPEFEFTSERSG--GAQOLQEELIVGSVAEVEMVVVVVIALVCLR--HORQPDAYIEECKOY--IA
 EphB3.h IDGLOPDARZVWVQVRAARTVAG--YCOYSRPEFEFTSERSG--GAQOLQEELIVGSATAILVSVVLLVIALVCLR--HORQPDSEYIEECKOY--IA
 34869730.m IDGLOPDARZVWVQVRAARTVAG--YCOYSRPEFEFTSERSG--GAQOLQEELIVGSVAEVEMVVVVVIALVCLR--HORQPDAYIEECKOY--VA
 40538750.d VEGIKAKPESVUQVRAARTVAG--YCFSKMFCOTLDDY--PERSVQDDELLVGSASAEVVILIMVIALVCLR--RTRGSELEYIEECKOY--VS
 18858599.d ISDURRQTOEVQVRAARTVAG--YCSFCKAIIIFPDLDE--DDSS-SPELVTCILLAMCMLLIVIICATVCTR--PNNYKQDEPSDKNGY--LNG
 18859329.d INDUSRAQSOQVQVRAARTVAG--YCHFSQAVSISPLSDD--EEESP-SRMILTCVLAQMLLILIVVAVVACFR--RSTRRDBD--DKSGOF--LNG
 31560596.m IRGKRGASYLVQVRAARSEAG--YCFPQEHHHSQTQDE--SESWREQHLLIAGVVVVLVLLVVVVIALVCLR--PQSNGREVEYSDKCGY--LIG
 EphB4.h IRGKRGASYLVQVRAARSEAG--YCFPQEHHHSQTQDE--SEGWREQHLLIAGTVVVCVLLVLLVVIWAVVIALVCLR--PQSNGREAEYSDKCGY--LIG
 31982461.n VTRSPGKVVFOVRAARTVAG--HCPYGGKVVFOVLPGE--LSSQLEPKSLVIG-SILCATAFLLLAITVIALV--FORKRRTGYIEECKOY--SPG
 EphB6.h VTRSPGKVVFOVRAARTVAG--HCPYGGKVVFOVLPGE--LSSQLEPKSLVIG-SILCATAFLLLAITVIALV--FORKRRTGYIEECKOY--SPG
 24308430.d VDGKPKPTIYIFVRAARTDGG--YNYKGEBELETSEED--MLAVGDINQQTILAIISVACCAVLLVLLVACFIVSG--RPGCITRAKQDFECKMCFQHG--RVKL
 24119222.d VDGKPKPTIYIFVRAARTDGG--YNYKGEBELETSEED--MIAIGGQNQSTIIVVLSVAGCIVVLLTDLVIVVFCVSG--RICGJTKAKQDFECKMCFQHG--RVKL
 34328113.m IKGHNPISTYVVFVQVRAARTVAG--YDFSEPVIEVNTV--SRIIGDGANSVTLVSVSGSVVLLVLLIAAFVI--RSKISKAKQDEADSEKHLNQG--
 EphA4.h IKGHNPISTYVVFVQVRAARTVAG--YDFSEPVIEVNTV--SRIIGDGANSVTLVSVSGSVVLLVLLIAAFVI--RSKISKAKQDEADSEKHLNQG--
 34876933.m IKGHNPISTYVVFVQVRAARTVAG--YDFSEPVIEVNTV--SRIIGDGANSVTLVSVSGSVVLLVLLIAAFVI--SRRTLIDHSGPSDVSLGRESDAAYVSRLPLRRSKISQAKQDEADSEKHLNQG--
 6679663.m VSGLKPATRYVVFQVRAARTSAG--CRFSAEVEETGK-R--PRYDITRIVWICLTHINGVLLVLLLICKKR--HCGVSKAQDSDDEKMHYQNGQAPPVFLPLNH--PPGKF
 34872126.m VSGLKPATRYMFCQVRAARTSAG--CRFSAEVEETGK-R--PRYDITRIVWICLTHINGVLLVLLLICKKR--HCGVSKAQDSDDEKMHYQNGQAPPVFLPLNH--PPGKL
 EphA8.h VSGLKPATRYVVFQVRAARTSAG--CRFSAEVEETGK-R--PRYDITRIVWICLTHINGVLLVLLLICKKR--HCGVSKAQDSDDEKMHYQNGQAPPVFLPLNH--PPGKL
 34328170.m INNLKPDTVYVFQVRAARTVAG--YNYSPRDLVTALEFASCKMFATAVSSEQNPVIIIAVVAVA-TIILVCMVFGFIIGR--RIGCGVSKADQECDFEE-LMF--HFKF
 19705437.m INNLKPDTVYVFQVRAARTVAG--YNYSPRDLVTALEFASCKMFATAVSSEQNPVIIIAVVAVA-TIILVCMVFGFIIGR--RIGCGVSKADQECDFEE-LMF--HFKF
 EphA7.h INNLKPDTVYVFQVRAARTVAG--YNYSPRDLVTALEFASCKMFATAVSSEQNPVIIIAVVAVA-TIILVCMVFGFIIGR--RIGCGVSKADQECDFEE-LMF--HFKF
 6679659.m AEGIKPASVYVFQVRAARTVAG--YVFSRREFEETTPVS--VAAENDQSIITAVSVTVVILLAVMIFLLEGS--CCDCGGGRASSLCAVAHPSLIMVCGVSKAKQDEESEKMHFNG--HIKL
 EphA5.h AEGIKPASVYVFQVRAARTVAG--YVFSRREFEETTPVS--AASS-DQSIITAVSVTVVILLAVMIFLLEGS--CCDCGGGRASSLCAVAHPSLIMVCGVSKAKQDEESEKMHFNG--HIKL
 34876735.m AEGIKPASVYVFQVRAARTVAG--YVFSRREFEETTPVS--VAAENDQSIITAVSVTVVILLAVMIFLLEGSSTWHYLPSFVAACCGCGRASSLCAVAHPSLIMVCGVSKAKQDEESEKMHFNG--HIKL
 13928766.m ISSLKPDTIYVFQVRAARTVAG--YTNRKKEFEFTSEDS--FSISGENSHVMIIASAVVIIIVT-YVLLGR--FCGIVHKSKHSDDERRIIFFGNG--HLRL
 34867401.m ISSLKPDTIYVFQVRAARTVAG--YTNRKKEFEFTSEDS--FSISGENSHVMIIASAVVIIIVT-YVLLGR--FCGIVHKSKHSDDERRIIFFGNG--HLRL
 31982448.m ISSLKPDTIYVFQVRAARTVAG--YTNRKKEFEFTSEDS--FSISGENSHVMIIASAVVIIIVT-YVLLGR--FCGIVHKSKHSDDERRIIFFGNG--HLKL
 EphA3.h ISSLKPDTIYVFQVRAARTVAG--YTNRKKEFEFTSEDS--FSISGENSHVMIIASAVVIIIVT-YVLLGR--FCGIVHKSKHSDDERRIIFFGNG--HLKL
 20893175.m VTKLKPATIYIFVIRVTAAG--YCGYSOKKEFEETGDT--SDMAAEQGQIIVVIAATAVGCFTLLVILITLFFLITTG--RCQWVTRAKMKSEEERRRHLQN--GHLRF
 6679661.m VTKLKPATIYIFVIRVTAAG--YCGYSOKKEFEETGDT--SDMAAEQGQIIVVIAATAVGCFTLLVILITLFFLITTG--RCQWVTRAKMKSEEERRRHLQN--GHLRF
 EphA6.h VTKLKPATKXVFIRVTAAG--YCGYSOKKEFEETGDT--SDMAAEQGQIIVVIAATAVGCFTLLVILITLFFLITTG--RCQWVTRAKMKSEEERRRHLQN--GHLRF
 34867994.m LT--LLHHLERVAVS--DMAAEQGQIIVVIAATAVGCFTLLVILITLFFLITTG--RCQWVTRAKMKSEEERRRHLQN--SHLRF
 34871174.m VTKLKPATRYVVFQVRAASPGPSWEAQSEPSSEIVDOPCEVAP--GSRDQSPAVVITVVISALLVLSVMVLAIVWR--ICD-GKGSQNAHDEEELYFH--FKV
 EphA10.h VTKLKPATRYVVFQVRAASPGPSWEAQSFNSIEVOLGEAAS--GSRDQSPAVVITVVISALLVLSVMVLAIVWR--PCSYGKGGGDADHEEELYFH--FKV

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| ← protein kinase domain .

protein kinase domain

1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 18

 17535165.w EVMIGYRIPPPMDCPGMLYRRAOWC KMERHRRPTEIOLLAFFRYILOPTLIEDPGELFRVQSOSAALNTYGSVNNGVVTTPSSAAPMSLDDFLRQLLNHVYCOLVSNNIHVSVDLANTSHL-DILAYGLMSAECSTVRDGLNCRISGSPPCGSSGT-IHATRGRTRTPP-REEGFFV-
 17535163.w EVMIGYRIPPPMDCPGMLYRRAOWC KMERHRRPTEIOLLAFFRYILOPTLIEDPGELFRVQSOSAALNTYGSVNNGVVTTPSSAAPMSLDDFLRQLLNHVYCOLVSNNIHVSVDLANTSHL-DILAYGLMSAECSTVRDGLNCRISGSPPCGSSGT-IHATRGRTRTPP-REEGFFV-
 31203311.i SIECGYRIPPPMDCPGMLYRRAOWC KMERHRRPTEIOLLAFFRYILOPTLIEDPGELFRVQSOSAALNTYGSVNNGVVTTPSSAAPMSLDDFLRQLLNHVYCOLVSNNIHVSVDLANTSHL-DILAYGLMSAECSTVRDGLNCRISGSPPCGSSGT-IHATRGRTRTPP-REEGFFV-
 32484983.m AINDCFRIPPPMDCPGMLYRRAOWC QQRERSRPPKEADIVSLLDKLIRAPDSIKLADFDIIRVSPGSTGS-EGVPFRTVSELESIMKMQYDEHFVVAICYTAIEKWWQMSNE-DIKRIGVR-LPGHOKK-IAYSLLGKLDQVNT-VGIPPI-
 34872522.m AINDCFRIPPPMDCPGMLYRRAOWC QQRERSRPPKEADIVSLLDKLIRAPDSIKLADFDIIRVSPGSTGS-EGVPFRTVSELESIMKMQYDEHFVVAICYTAIEKWWQMSNE-DIKRIGVR-LPGHOKK-IAYSLLGKLDQVNT-VGIPPI-
 EphA2.h AINDCFRIPPPMDCPGMLYRRAOWC QQRERSRPPKEADIVSLLDKLIRAPDSIKLADFDIIRVSPGSTGS-EGVPFRTVSELESIMKMQYDEHFVVAICYTAIEKWWQMSNE-DIKRIGVR-LPGHOKK-IAYSLLGKLDQVNT-VGIPPI-
 34855604.m SIECGYRIPPPMDCPGMLYRRAOWC AYDRARRPPEFLQDQALQLEQLLDPISLRIRANFDRVLRPLPSLSGS-DGIPYPSVSELESIMKRYIIHFSACADTMECVLELTAB-DITQMGIT-LPGHOKK-IIICSIQGRKD-
 31980651.m SIECGYRIPPPMDCPGMLYRRAOWC AYDRARRPPEFLQDQALQLEQLLDPISLRIRANFDRVLRPLPSLSGS-DGIPYPSVSELESIMKRYIIHFSACADTMECVLELTAB-DITQMGIT-LPGHOKK-IIICSIQGRKD-
 EphA1.h SIECGYRIPPPMDCPGMLYRRAOWC AYDRARRPPEFLQDQALQLEQLLDPISLRIRANFDRVLRPLPSLSGS-DGIPYPSVSELESIMKRYIIHFSACADTMECVLELTAB-DITQMGIT-LPGHOKK-IIICSIQGRKD-
 38078900.m AIECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNSLKAMAPLSSGGNLPILLDRTP-DYTFSEITVDEMLAEAKMCGYKESFNAACFTSEDVVSQMMB-DILRIGVIT-LAGHOKK-IIINSIQVMAONQ-IQSVEV-
 EphB2.h AIECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNSLKAMAPLSSGGNLPILLDRTP-DYTFSEITVDEMLAEAKMCGYKESFNAACFTSEDVVSQMMB-DILRIGVIT-LAGHOKK-IIINSIQVMAONQ-IQSVEVQPLARRFRATGR-
 34872119.m AIECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNSLKAMAPLSSGGNLPILLDRTP-DYTFSEITVDEMLAEAKMCGYKESFNAACFTSEDVVSQMMB-DILRIGVIT-LAGHOKK-IIINSIQVMAONQ-IQSVEV-
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 27721289.m AIECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNASLKVATITAVS-SQPLLDRSIP-DFTAFITVDDMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IISSITMSRVMONQ-SPSVM-
 40254274.m AIECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNASLKVATITAVS-SQPLLDRSIP-DFTAFITVDDMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IISSITMSRVMONQ-SPSVM-
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 33859548.m AVECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNASLKVATASAPSQNSQPLLDRTV-DYTFITVDEDMLDAIKMGRYKESFVGACFAEDIVAQMTSF-DILRIGVIT-LAGHOKK-IISSITDMRLQONQ-3LPQV-
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 34869730.m AVECDYRIPPPMDCPGMLYRRAOWC QKDRNRPKEFGQIVNLDDKMRNPNASLKVATASAPSQNSQPLLDRTV-DYTFITVDEDMLDAIKMGRYKESFVGACFAEDIVAQMTSF-DILRIGVIT-LAGHOKK-IISSITDMRLQONQ-3LPQV-
 40538750.d AVECDYRIPPPMDCPGMLYRRAOWC VIKERNRPKEFGQIVNLDDKMRNPNASLKVATITAVS-SQPLLDRTV-DFTAFITVDDMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IISSITDMRLQONQ-3LPQV-
 18858599.m AIECDYRIPPPDCSTYLHOLMLDC QKERTSRPREATIVNLSLDLIRRNPAISLKAT-DEGAGSHPLLDQSPFL-TPSSCTVCDMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IISSITACGIONKA-PGVNLVY-
 18859329.d AIECDYRIPPPDCPASLHOLMLDC QKERSRPRECATIVNLDLIRRNPAISLKAT-TRIPDGSHPLLDQAPP-PLSSCQSVNDMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IISSVCTERIGHG-GSLRY-
 31560596.m AIECDYRIPPPDCPNSLHOLMLDC QKDRNRPKEFGQIVNLDDKMRNPNASLKVATENGGASHPLLDQRP-HYSAFCSVEMMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IIASVCHMKSQAKPGAPGGTGGPAQQF-
 EphB4.h AIECDYRIPPPDCPNSLHOLMLDC QKDRNRPKEFGQIVNLDDKMRNPNASLKVATENGGASHPLLDQRP-HYSAFCSVEMMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IIASVCHMKSQAKPGTPGGTGGPAQQF-
 31982461.m AIECDYRIPPPDCPQCLHMLDT QKDRARRPHEPDOLVAAFKDMIRKPDTLQEGGSDRISQALINNVAL-DFCLDSQPAQMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IIENIGLQOQDRLQ-PGSVEV-
 EphB6.h AIECDYRIPPPDCPQCLHMLDT QKDRARRPHEPDOLVAAFKDMIRKPDTLQEGGDPGEPSQALINNVAL-DFCLDSQPAQMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DILRIGVIT-LAGHOKK-IIENIGLQOQDRLQ-QGSVEV-
 24308430.d AVDEGYRIPAPMDCPVVLHOLMLDC EKNRNRPKEFGQIVNLDDKMRNPNSSLQLLAN--SAVEDD-PVTPEAAVNTVDEDLIMCGYKEHFISAYVVLDELVVYSS-ELDKRIGVIT-LAGHOKK-IISSIOCIC-QAHHGTQV-
 24119222.d AIECDYRIPAPMDCPVVLHOLMLDC EKNRNRPKEFGQIVNLDDKMRNPNSSLQLLAN--SSVEDD-PTTTEFSSTVDEMLDAINQYKDNFNAVYSLDDILNIMC-EDSKNDVIT-LPGHOKK-IISSAVCQ-HAAG-THVQV-
 34328113.m AIEEGYRIPPPMDCPALHOLMLDC QKERSRPRECATIVNLDLIRRNPNSLKRTGTGESSRNTALLD-PSSSEFSAVSVWDLQAIKMKYRDNFIAACYYTILEAVVVRNNE-DIARIGIT-AITHONK-IISSVCAWMTQONQMHGRMV-
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 34876933.m AIEEGYRIPPPMDCPALHOLMLDC QKERSRPRECATIVNLDLIRRNPNSLKRTGTGESSRNTALLD-PSSSEFSAVSVWDLQAIKMKYRDNFIAACYYTILEAVVVRNNE-DIARIGIT-AITHONK-IISSVCAWMTQONQMHGRMV-
 66796633.m SVEEGYRIPAPMCPRALHOLMLDC HKDRAPRPREATIVVSLDVTSPESLRATITVSRCPPPAFARSQFDL-RAGGSGNGDITVCDMLDSIMRGRYRHFAGCYSSLCMVRMRNAC-DVRLIGVIT-LMGHOKK-IISSITMRALQASSQGRRL-
 34872126.m SVEEGYRIPAPMCPRALHOLMLDC HKDRAPRPRESHVVSLELVLVSPESLPAITAVSRCPAPAFARSQFDL-RAGGNGNGDITVCDMLDSIMRGRYRHFAGCYSSLCMVRMRNAC-DVRLIGVIT-LMGHOKK-IISSITMRALQSCSQGRRL-
 EphA8.h SVEEGYRIPAPMCPRALHOLMLDC HKDRAPRPRESHVVSLELVLVSPESLPAITAVSRCPAPAFARSQFDL-RGGSGGGGQITVCDMLDSIMRGRYRHFAGCYSSLCMVRMRNAC-DVRLIGVIT-LMGHOKK-IISSITMRALQSTSQGRRL-
 34328170.m AIEEGYRIPAPMDCPALHOLMLDC QKDRAPRKEQIVVGLDDKMRNPNPSLKLPLTCSPRLPSLLD-QSTEDFATFASVEMMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DVMSLGIT-LPGHOKK-IMSSITMRALQMLHLHGTTGICV-
 19705437.m AIEEGYRIPAPMDCPALHOLMLDC QKDRAPRKEQIVVGLDDKMRNPNPSLKLPLTCSPRLPSLLD-QSTEDFATFASVEMMLSAIKMVQYRDSFLTAFTSLQVVTQMTSF-DVMSLGIT-LPGHOKK-IMSSITMRALQMLHLHGTTGICV-
 EphA7.h 6679659.m AVEEGYRIPAPMDCPAALYHOLMLDC QKDRNRPKEFOIVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-QNTEDFTTFSVSEMLQAIKMKYRDNFIAACYYTILEAVVVRNNE-DVRLIGVIT-LPGHOKK-IMSSITMRALQMLHLHGTTGICV-
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 34876735.m AVEEGYRIPAPMDCPAALYHOLMLDC QKDRNRPKEFOIVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-HSLGSGCAYSVCEMLSAIKMKYRDNFIAACYYTILEAVVVRNNE-DVRLIGVIT-LPGHOKK-IMSSIKATEOSKNGP-VV-
 13928766.m AVDEGYRIPPLPMDCPAALYHOLMLDC QKDRNRPKEFOIVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-QSNVDIATFETTCDMLNGMRTAHCKEIFTFGVYSSCDIAKISID-DNKKVGVIT-VVGHOKK-IISSIKATEOSKNGP-VV-
 34867401.m AVDEGYRIPPLPMDCPAALYHOLMLDC QKDRNRPKEFOIVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-QSNVDIATFETTCDMLNGMRTAHCKEIFTFGVYSSCDIAKISID-DNKKVGVIT-VVGHOKK-IISSIKATEOSKNGP-VV-
 31982448.m AVDEGYRIPPPMDCPAALYHOLMLDC QKDRNRPKEFOIVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-QSNVDIATFETTCDMLNGMRTAHCKEIFTFGVYSSCDIAKISID-DNKKVGVIT-VVGHOKK-IIISTIKATEOSKNGP-VV-
 EphA3.h AVDEGYRIPPPMDCPAALYHOLMLDC QKDRNRPKEFOIVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-QSNVDIATFETTCDMLNGMRTAHCKEIFTFGVYSSCDIAKISID-DNKKVGVIT-VVGHOKK-IISSIKATEOSKNGP-VV-
 20893175.m SIEEGYRIPAPMCPSLHOLMLDC QKERNRPKEFTDITVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-VIEYLFITVCDMLDSIMRGRYRHFAGCYSSLCMVRMRNAC-DVRLIGVIT-LIGHORR-IVSSICOTRLHMHIQEKGFIV-
 6679661.m SIEEGYRIPAPMCPSLHOLMLDC QKERNRPKEFTDITVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-VIEYLFITVCDMLDSIMRGRYRHFAGCYSSLCMVRMRNAC-DVRLIGVIT-LIGHORR-IVSSICOTRLHMHIQEKGFIV-
 EphA6.h SIEEGYRIPAPMCPSLHOLMLDC QKERNRPKEFTDITVNLDDKMRNPNSLKGLPGLTCSPRLPSLLD-VIEYLFITVCDMLDSIMRGRYRHFAGCYSSLCMVRMRNAC-DVRLIGVIT-LIGHORR-IVSSICOTRLHMHIQEKGFIV-
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 34871174.m .LHLMLEC QKEDPGRPRFESQIHSLSKMGKCEPEPSKCASTTCRPTPFAADRAFS-AFSSFSVSEMLSAIKMKYRDNFIAACYYTILEAVVVRNNE-DILGSLGIS-SABHRALLSGTIALQDTPFPFTLLPGHLTSDLCRNT-
 EphA10.h AVEDCFRIPPPRNCPNULHOLMLDC QKDPGPFRPESQIHSLSKMWVDPBEPPKCALTTCPRTPFAADRAFS-TFSPSFVSEMLSAIKMKYRDNFIAACYYTILEAVVVRNNE-DABHRALLSGTIALQDTPFPFTLLPGHLTSDLCRNT-

• • protein kinase → |

| ← Sterile alpha motif (SAM) → |

